

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 21:44:35 ; Search time 223 Seconds
(without alignments)
397.337 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|---------------|-------|-------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 1268 | 100.0 | 247 | 2 | AAR84522 | Aar84522 Stannioca |
| 2 | 1268 | 100.0 | 247 | 3 | AAB23264 | Aab23264 Human sta |
| 3 | 1268 | 100.0 | 247 | 3 | AA55750 | Aay55750 Human sta |
| 4 | 1268 | 100.0 | 247 | 3 | AA57166 | Aay57166 Human cor |
| 5 | 1268 | 100.0 | 247 | 3 | AA92901 | Aay92901 Human sta |
| 6 | 1268 | 100.0 | 247 | 4 | AAB62473 | Aab62473 Human sta |
| 7 | 1268 | 100.0 | 247 | 4 | AAB62690 | Aab62690 Lng108, a |
| 8 | 1268 | 100.0 | 247 | 5 | ABB06259 | Abb06259 Human sta |
| 9 | 1268 | 100.0 | 247 | 6 | ABP97748 | Abp97748 Amino aci |

| | | | | | | | |
|----|-------|-------|-----|---|----------|----------|-----------|
| 10 | 1268 | 100.0 | 247 | 6 | ABR47600 | Abr47600 | Breast ca |
| 11 | 1268 | 100.0 | 247 | 6 | ABG72290 | Abg72290 | Human Cor |
| 12 | 1268 | 100.0 | 247 | 7 | ADD48082 | Add48082 | Human Pro |
| 13 | 1268 | 100.0 | 247 | 7 | ADI30575 | Adi30575 | Human sta |
| 14 | 1268 | 100.0 | 247 | 7 | ABO84399 | Abo84399 | Human sta |
| 15 | 1268 | 100.0 | 247 | 8 | ADQ21382 | Adq21382 | Human sof |
| 16 | 1231 | 97.1 | 247 | 7 | ADD48080 | Add48080 | Rat Prote |
| 17 | 937 | 73.9 | 276 | 3 | AAB56848 | Aab56848 | Human pro |
| 18 | 680.5 | 53.7 | 261 | 1 | AAP82968 | Aap82968 | Corpuscle |
| 19 | 662.5 | 52.2 | 256 | 4 | AAB62474 | Aab62474 | Coho salm |
| 20 | 628 | 49.5 | 170 | 3 | AAy55749 | Aay55749 | A. austra |
| 21 | 628 | 49.5 | 170 | 7 | ADI30574 | Adi30574 | Australia |
| 22 | 358 | 28.2 | 70 | 4 | AAM18134 | Aam18134 | Peptide # |
| 23 | 358 | 28.2 | 70 | 4 | ABB37166 | Abb37166 | Peptide # |
| 24 | 358 | 28.2 | 70 | 4 | AAM30637 | Aam30637 | Peptide # |
| 25 | 358 | 28.2 | 70 | 4 | ABB31928 | Abb31928 | Peptide # |
| 26 | 358 | 28.2 | 70 | 4 | ABB22472 | Abb22472 | Protein # |
| 27 | 358 | 28.2 | 70 | 4 | AAM70300 | Aam70300 | Human bon |
| 28 | 358 | 28.2 | 70 | 4 | AAM57878 | Aam57878 | Human bra |
| 29 | 358 | 28.2 | 70 | 4 | ABG52000 | Abg52000 | Human liv |
| 30 | 358 | 28.2 | 70 | 4 | AAM05763 | Aam05763 | Peptide # |
| 31 | 358 | 28.2 | 70 | 5 | ABG39940 | Abg39940 | Human pep |
| 32 | 354.5 | 28.0 | 296 | 3 | AAy67926 | Aay67926 | Mouse sta |
| 33 | 354.5 | 28.0 | 296 | 4 | AAB61623 | Aab61623 | Murine st |
| 34 | 354 | 27.9 | 293 | 2 | AAy41255 | Aay41255 | Adipogene |
| 35 | 354 | 27.9 | 293 | 3 | AAB26872 | Aab26872 | Human adi |
| 36 | 354 | 27.9 | 293 | 4 | AAB93965 | Aab93965 | Human pro |
| 37 | 354 | 27.9 | 302 | 3 | AAy67925 | Aay67925 | Human sta |
| 38 | 354 | 27.9 | 302 | 4 | AAB98971 | Aab98971 | Human adi |
| 39 | 354 | 27.9 | 302 | 4 | AAB61621 | Aab61621 | Human sta |
| 40 | 354 | 27.9 | 302 | 4 | AAB31797 | Aab31797 | Amino aci |
| 41 | 354 | 27.9 | 302 | 4 | AAB95330 | Aab95330 | Human pro |
| 42 | 354 | 27.9 | 302 | 5 | ABJ05546 | Abj05546 | Breast ca |
| 43 | 354 | 27.9 | 302 | 5 | AAE26113 | Aae26113 | Human BS2 |
| 44 | 354 | 27.9 | 302 | 6 | ABR47601 | Abr47601 | Breast ca |
| 45 | 354 | 27.9 | 302 | 6 | ADA00844 | Ada00844 | Human bre |

ALIGNMENTS

RESULT 1

AAR84522

ID AAR84522 standard; protein; 247 AA.

XX

AC AAR84522;

XX

DT 19-APR-1996 (first entry)

XX

DE Stanniocalcin from Corpuscles of Stannius.

XX

KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;

KW electrolyte disorder; osteoporosis; Paget's disease; treatment.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .33
 FT /label= prepro_region
 FT Protein 34. .247
 FT /label= mature_stanniocalcin
 XX
 PN WO9524411-A1.
 XX
 PD 14-SEP-1995.
 XX
 PF 09-MAY-1994; 94WO-US005136.
 XX
 PR 08-MAR-1994; 94US-00208005.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen H, Adams MD;
 XX
 DR WPI; 1995-328227/42.
 DR N-PSDB; AAT02438.
 XX
 PT Human corpuscles of Stannius polypeptide(s) - used to treat
 PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.
 XX
 PS Claim 14; Fig 1; 4lpp; English.
 XX
 CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
 CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
 CC used for the treatment of e.g. electrolyte disorders which lead to renal,
 CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
 CC to elevated bone resorption, e.g. osteoporosis and Paget's disease
 XX
 SQ Sequence 247 AA;

Query Match . 100.0%; Score 1268; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| | | | |
| Db | 1 | MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD | 180 |
| | | | |
| Db | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD | 180 |
| Qy | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK | 240 |
| | | | |
| Db | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK | 240 |
| Qy | 241 | RTSHESA 247 | |
| | | | |
| Db | 241 | RTSHESA 247 | |

AAB23264

XX

XX

XX

XX

KW mineral metabolism regulator; prophylaxis; therapy.

XX

XX

XX

XX

XX

XX

XX

DR N-PSDB; AAA97594.

XX

XX

XX

XX

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

Db

Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
 |||||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
 |||||

Db 241 RTSHESA 247

RESULT 3

AA55750

ID AAY55750 standard; protein; 247 AA.

XX

AC AAY55750;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human stanniocalcin polypeptide.

XX

KW Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
 KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
 KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
 KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
 KW Paget's disease; hypercalcemia.

XX

OS Homo sapiens.

XX

PN US5994103-A.

XX

PD 30-NOV-1999.

XX

PF 02-JUN-1995; 95US-00460529.

XX

PR 10-NOV-1994; 94WO-US013206.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Fleischmann RD, Olsen HS;

XX

DR WPI; 2000-038260/03.

XX

PT Isolated nucleic acids encoding human stanniocalcin-alpha useful for
 PT treating electrolyte disorders which lead to renal, bone and heart
 PT diseases, osteoporosis and Paget's disease.

XX

PS Disclosure; Fig 3; 21pp; English.

XX

CC The invention provides a human stanniocalcin-alpha polypeptide (also
 CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
 CC hypercalcemic glycoprotein hormone produced by the corpuscles of
 CC stannius. It has a similar reported biological activity to that of
 CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
 CC in mammals. They exert hypercalcemic activity due to stimulation of bone
 CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
 CC at low doses it increases bone formation and at high doses it increases

CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC of it (under different circumstances) may be used to treat osteoporosis.
CC The DNA may be used to produce human stanniocalcin-alpha according to
CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC be produced either in vitro in a fermentation culture or in vivo as part
CC of a gene therapy protocol, and may be used to treat electrolyte
CC disorders which lead to renal, bone and heart diseases. Due to the
CC biphasic nature of stanniocalcin-alpha it may be used to treat
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC polypeptides may be used as antigens in the production of antibodies to
CC stanniocalcin-alpha and to assay for agonists and antagonists of its
CC activity. The antibodies and antagonists may be used to inhibit the
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC hypercalcemia. The present sequence represents a human stanniocalcin

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120

Qy    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKvLLRNLRGEEDSPSHIK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKvLLRNLRGEEDSPSHIK 240

Qy    241 RTSHESA 247
          |||||||
Db    241 RTSHESA 247
```

RESULT 4

AA57166

ID AAY57166 standard; protein; 247 AA.

XX

AC AAY57166;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human corpuscles of staninus polypeptide.

XX

KW Corpuscles of staninus polypeptide; calcium; inhibition; human; renal;
KW therapeutic; bone; heart disease; hypocalcemia; osteopetrosis.

XX

OS Homo sapiens.

XX

PN US5994301-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 28-APR-1995; 95US-00431117.
 XX
 PR 08-MAR-1994; 94US-00208005.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Adams MD, Olsen HS;
 XX
 DR WPI; 2000-038269/03.
 DR N-PSDB; AAZ39520.
 XX
 PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.
 XX
 PS Claim 4; Fig 1A-B; 23pp; English.
 XX
 CC This represents a human corpuscles of stanius polypeptide, having a
 CC calcium uptake inhibitory activity. The cDNA is deposited under the
 CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
 CC method for the treatment of a patient having need to inhibit uptake of
 CC calcium. The method is also used for the therapeutic treatment of renal,
 CC bone, and heart diseases, and the antagonist (may be an antibody) may be
 CC used for treating hypocalcemia., and osteoperosis
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| | | | |
| Db | 1 | MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS | 180 |
| | | | |
| Db | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS | 180 |
| Qy | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVL | 240 |
| | | | |
| Db | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVL | 240 |
| Qy | 241 | RTSHESA | 247 |
| | | | |
| Db | 241 | RTSHESA | 247 |

RESULT 5
 AAY92901
 ID AAY92901 standard; protein; 247 AA.

XX
 AC AAY92901;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Human stanniocalcin protein.
 XX
 KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
 KW adipocyte; obesity; diabetes; hypertension; heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200016795-A1.
 XX
 PD 30-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-JP005080.
 XX
 PR 17-SEP-1998; 98JP-00263004.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;
 XX
 DR WPI; 2000-283445/24.
 DR N-PSDB; AAA11145.
 XX
 PT Treating or preventing obesity, which is a risk factor for diabetes,
 PT hypertension and heart disease, comprises administering an agent
 PT containing stanniocalcin.
 XX
 PS Example 1; Page 16; 19pp; Japanese.
 XX
 CC This sequence represents the human stanniocalcin protein. Stanniocalcin
 CC is an inhibitor of the differentiation and maturation of adipocytes. The
 CC protein is used for preventing and treating obesity which is a risk
 CC factor for diabetes, hypertension, and heart disease. The coding sequence
 CC was isolated from IMR-90 cells
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAQNSAEVVRCLNSALQVGC | 60 |
| | | | |
| Db | 1 | MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAQNSAEVVRCLNSALQVGC | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRR | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRR | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLL | 180 |
| | | | |
| Db | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLL | 180 |

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
 |||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
 |||||
 Db 241 RTSHESA 247

RESULT 6

AAB62473

ID AAB62473 standard; protein; 247 AA.

XX

AC AAB62473;

XX

DT 09-JUL-2001 (first entry)

XX

DE Human stanniocalcin (STC) protein.

XX

KW Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
 KW antirheumatic; antiarthritic; dermatological; antiallergic; human;
 KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
 KW antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
 KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
 KW hemostatic; thrombolytic.

XX

OS Homo sapiens.

XX

PN WO200130969-A2.

XX

PD 03-MAY-2001.

XX

PF 20-OCT-2000; 2000WO-US029432.

XX

PR 27-OCT-1999; 99US-0161740P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UYHE-) UNIV HELSINKI.

XX

PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;
 PI Andersson LC;

XX

DR WPI; 2001-308626/32.

DR N-PSDB; AAF83297.

XX

PT.. Novel composition useful for treating or protecting neural cells, for
 PT treating Addison's disease, organ rejection, hyperproliferative disorder,
 PT cancer, AIDS, multiple sclerosis, comprises stanniocalcin polypeptide.

XX

PS Claim 1; Fig 1A-C; 253pp; English.

XX

CC The invention relates to a human stanniocalcin (STC) polypeptide. A
 CC pharmaceutical composition comprising the STC is useful for treating a
 CC patient in need of increased levels of STC activity. STC and its
 CC modulators are useful for treating disorders or abnormalities of nervous
 CC system, cerebrovascular diseases, dementia, encephalitis, central nervous
 CC system infections or neoplasms, demyelinating diseases,

CC encephalomyelitis, spinal cord diseases, mental retardation such as
 CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
 CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
 CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
 CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
 CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
 CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
 CC reactions and conditions such as asthma, for treating and/or preventing
 CC organ rejection or graft-versus-host disease, hyperproliferative diseases
 CC such as purpura, Gaucher's disease, cardiovascular disorders such as
 CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
 CC disorders with neovascularization. The composition can be used to treat
 CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
 CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
 CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
 CC or detecting infectious agents. The present sequence represents the human
 CC STC polypeptide

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTS HESA 247
 |||||
 Db 241 RTS HESA 247

RESULT 7

AAB62690

ID AAB62690 standard; protein; 247 AA.

XX

AC AAB62690;

XX

DT 06-AUG-2001 (first entry)

XX

DE Lng108, a diagnostic marker for cancer.

XX

KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.

XX
 OS Homo sapiens.
 XX
 PN WO200132209-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US030482.
 XX
 PR 04-NOV-1999; 99US-0163444P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Recipon H, Macina RA, Chen S, Sun Y;
 XX
 DR WPI; 2001-316386/33.
 DR N-PSDB; AAF83823.
 XX
 PT Novel assay for diagnosing and monitoring cancer, involves determining
 PT levels of Lngl08 in cells, tissues or bodily fluids of the patient, and
 PT comparing with control.
 XX
 PS Disclosure; Page 33-34; 36pp; English.
 XX
 CC The invention relates to diagnosing the presence of cancer or diagnosing
 CC metastases of cancer in a patient that involves determining levels of
 CC Lngl08 in a sample of cells, tissues or bodily fluids in a patient, and
 CC comparing the determined levels with levels of Lngl08 a normal human
 CC control. The method is useful for diagnosing the presence of cancer,
 CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
 CC monitoring a change in stage of the cancer, in a patient. A therapeutic
 CC agent which is an antibody labeled with paramagnetic ions or a
 CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
 CC cancer in a patient. A molecule which downregulates the expression or
 CC activity of Lngl08, is useful for treating cancer in a patient. Lngl08
 CC protein is useful for inducing an immune response against a target cell
 CC expressing Lngl08. The present sequence represents the human Lngl08
 CC polypeptide
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MLQNSAVLLVLVISASATHEAEQNDSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACL | 60 |
| | | | |
| Db | 1 | MLQNSAVLLVLVISASATHEAEQNDSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACL | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDedTVSTIRD | 180 |
| | | | |
| Db | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDedTVSTIRD | 180 |

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
 |||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
 |||
 Db 241 RTSHESA 247

RESULT 8

ABB06259

ID ABB06259 standard; protein; 247 AA.

XX

AC ABB06259;

XX

DT 23-MAY-2002 (first entry)

XX

DE Human staniocalcin 1 protein.

XX

KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
 KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
 KW rheumatic bone disease; cancer associated bone disease; rachitis;
 KW arthritis deformans.

XX

OS Homo sapiens.

XX

PN WO200204013-A1.

XX

PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-JP005962.

XX

PR 11-JUL-2000; 2000JP-00209926.

XX

PA (BMLB-) BML INC.

XX

PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;

XX

DR WPI; 2002-164600/21.

DR N-PSDB; ABL40225.

XX

PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
 PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
 PT with cancer and arthritis deformans containing staniocalcin I.

XX

PS Claim 2; Fig 1; 24pp; Japanese.

XX

CC The present invention describes an agent containing staniocalcin 1,
 CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
 CC The agent can be used for treating diseases relating to osteogenesis
 CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
 CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
 CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
 CC rachitis and arthritis deformans. The agent increases bone mass. The
 CC present sequence represents human staniocalcin 1

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy    241 RTSHESA 247
        |||||
Db    241 RTSHESA 247
```

RESULT 9

ABP97748

ID ABP97748 standard; protein; 247 AA.

XX

AC ABP97748;

XX

DT 28-MAY-2003 (first entry)

XX

DE Amino acid sequence of human STC1 polypeptide.

XX

KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mig-6; SSR4;
KW cancer.

XX

OS Homo sapiens.

XX

PN WO2003010205-A1.

XX

PD 06-FEB-2003.

XX

PF 26-JUL-2002; 2002WO-US023786.

XX

PR 26-JUL-2001; 2001US-0307600P.

PR 24-JUL-2002; 2002US-00201642.

XX

PA (UYDU-) UNIV DUKE MEDICAL CENT.

XX

PI Riggins GJ, Lal A;

XX

DR WPI; 2003-239423/23.

DR N-PSDB; ABZ77288.

XX

PT Inhibiting angiogenesis for treating wound healing, retinopathy,
PT ischemia, inflammation, microvasculopathy, bone healing, skin
PT inflammation or follicular development by providing to a subject an
PT antisense polynucleotide.

XX

PS Claim 4; Page 61; 66pp; English.

XX

CC The present sequence is a human STC1 polypeptide. It is used in the
CC method of the invention. The specification describes a method modulating
CC angiogenesis associated with wound healing, retinopathy, ischemia,
CC inflammation, microvasculopathy, bone healing, skin inflammation or
CC follicular development. The method comprises providing to a subject HOG3,
CC HOG8, HOG18, CA9, HXB, IGFBP5, HFARP, STC1, mig-6 or SSR4. The methods,
CC antisense polynucleotides, polypeptides and antibodies are useful for
CC treating wound healing, retinopathy, ischemia, inflammation,
CC microvasculopathy, bone healing, skin inflammation or follicular
CC development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGCGAFACL 60
|||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy .61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFORM 120
|||||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFORM 120

Qy 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180
|||||

Db 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
|||||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||||

Db 241 RTSHESA 247

RESULT 10

ABR47600

ID ABR47600 standard; protein; 247 AA.

XX

AC ABR47600;

XX

DT 12-JUN-2003 (first entry)

XX

DE Breast cancer associated protein sequence SEQ ID NO:441.

XX
 KW Human; breast cancer; cytostatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003004989-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019669.
 XX
 PR 21-JUN-2001; 2001US-0299887P.
 PR 27-JUN-2001; 2001US-0301572P.
 PR 18-JUL-2001; 2001US-0306501P.
 PR 25-SEP-2001; 2001US-0325002P.
 PR 05-MAR-2002; 2002US-0362585P.
 PR 14-MAY-2002; 2002US-0380391P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
 XX
 DR WPI; 2003-210381/20.
 DR N-PSDB; ACC50301.
 XX
 PT Breast cancer diagnosis or treatment by comparing the level of expression
 PT of a marker in a patient sample with that in the control non-breast
 PT cancer sample.
 XX
 PS Claim 1; SEQ ID NO 441; 128pp; English.
 XX
 CC The present invention describes a method for assessing whether a patient
 CC is afflicted with breast cancer. The method comprises comparing the level
 CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
 CC ABR47386 to ABR47632) in a patient sample and the normal level of
 CC expression of the marker in a control non-breast cancer sample, where a
 CC significant increase in the level of expression of the marker in the
 CC patient sample and the normal level is an indication that the patient is
 CC afflicted with breast cancer. The breast cancer associated sequences from
 CC the present invention have cytostatic activities and can be used in gene
 CC therapy. The method is useful for diagnosing and treating breast cancer.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDVSPRKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLQNSAVLLVLVISASATHEAEQNDVSPRKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120
 |||||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
 |||||
 Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
 |||||
 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
 |||||
 Db 241 RTSHESA 247

RESULT 11

ABG72290

ID ABG72290 standard; protein; 247 AA.

XX

AC ABG72290;

XX

DT 14-MAR-2003 (first entry)

XX

DE Human Corpuscles of Stannius protein.

XX

KW Human; Corpuscles of Stannius protein; calcium uptake inhibitor;

KW renal excretion of phosphate; electrolyte disorder; renal disease;

KW bone disease; heart disease; arterial hypertension; bone resorption;

KW osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism;

KW hypervitaminosis D; tumour; serum calcium level; sarcoidosis;

KW hyperthyroidism; adrenal insufficiency; serum albumin; plasma protein;

KW GI calcium absorption; stanniocalcin; osteopathic; cytostatic;

KW hypotensive.

XX

OS Homo sapiens.

XX

PN US2002146791-A1.

XX

PD 10-OCT-2002.

XX

PF 05-APR-2002; 2002US-00116051.

XX

PR 08-MAR-1994; 94US-00208005.

PR 28-APR-1995; 95US-00431117.

PR 17-MAY-1999; 99US-00312610.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Olsen HS, Adams MD;

XX

DR WPI; 2003-147579/14.

DR N-PSDB; ABX15152.

XX

PT Isolated polynucleotide for encoding polypeptides used to diagnose and
 PT treat electrolyte disorders leading to renal disease, e.g. Paget's

XX

XX

cc

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

Db

Db

Db

ADD48082

ID ADD48082 standard; protein; 247 AA.

XX

XX

DT

XX

DE

XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P52823.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLQNSAVLLVLVISASATHEAEQNDSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQNSAVLLVLVISASATHEAEQNDSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy    121 IAEVQEECYSKLNVCSI AKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IAEVQEECYSKLNVCSI AKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy    241 RTSHESA 247
        |||||||
Db    241 RTSHESA 247
```

RESULT 13

ADI30575

ID ADI30575 standard; protein; 247 AA.

XX

AC ADI30575;

XX

DT 22-APR-2004 (first entry)

XX

DE Human stannioalcalcin protein:

XX

KW human; stannioalcalcin-alpha; electrolyte imbalance; hypertension;

KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;

KW osteoporosis; hypoglycaemia; Paget's disease.

XX

OS Homo sapiens.

XX

PN US2003181663-A1.

XX

PD 25-SEP-2003.

XX

PF 18-APR-2003; 2003US-00418226.

XX

PR 10-NOV-1994; 94WO-US013206.

PR 02-JUN-1995; 95US-00460529.

PR 28-JUL-1999; 99US-00361736.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Olsen HS, Fleischmann RD;

XX

DR WPI; 2003-852260/79.

XX

PT New human stanniocalcin-alpha polypeptide, useful in regulating
PT electrolyte imbalances, or for diagnosing and treating a disease
PT associated with mutated forms of stanniocalcin-alpha sequences, e.g.
PT renal disease or osteoporosis.

XX

PS Disclosure; SEQ ID NO 10; 22pp; English.

XX

CC The invention comprises the amino acid and coding sequence of a human
CC stanniocalcin-alpha protein. The DNA and protein sequences of the
CC invention are useful for regulating electrolyte imbalances to treat
CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences
CC are also useful in diagnosing and treating a disease associated with
CC mutated forms of stannicoalcin-alpha sequences, such as: renal disease,
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC present amino acid sequence represents a human stannicoalcin protein.

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;

Best Local Similarity 100.0%; Pred. No. 9.3e-124;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60

|||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120

|||||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIakRNPEAITEVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

|||||

Db 121 IAEVQEECYSKLNVCSIakRNPEAITEVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKvLLRNLRGEEDSPSHIK 240

|||||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKvLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247

|||||

Db 241 RTSHESA 247

RESULT 14

ABO84399

ID ABO84399 standard; protein; 247 AA.

XX

AC ABO84399;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human stanniocalcin protein.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection.

XX

OS Homo sapiens.

XX

PN WO200285309-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013143.

XX

PR 24-APR-2001; 2001US-0286036P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-093058/08.

DR N-PSDB; ABD20997.

XX

PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

XX

PS Claim 15; SEQ ID NO 6; 763pp; English.

XX

CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

XX
 PI Aziz N, Ginsburg WM, Zlotnik A;
 XX
 DR WPI; 2004-441208/41.
 XX
 PT Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.
 XX
 PS Example 2; SEQ ID NO 4202; 210pp; English.
 XX
 CC The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 8; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| | | | |
| Db | 1 | MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRCLNSALQVGC | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD | 180 |
| | | | |
| Db | 121 | IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD | 180 |
| Qy | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK | 240 |
| | | | |
| Db | 181 | SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK | 240 |
| Qy | 241 | RTSHESA | 247 |
| | | | |
| Db | 241 | RTSHESA | 247 |

Search completed: January 14, 2005, 22:14:51
 Job time : 235 secs

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OM protein - protein search, using sw model

Run on: January 14, 2005, 22:10:59 ; Search time 40 Seconds
(without alignments)
409.514 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|-------------------|
| 1 | 1268 | 100.0 | 247 | 2 | US-08-208-005C-2 | Sequence 2, Appli |
| 2 | 1268 | 100.0 | 247 | 2 | US-09-038-597A-2 | Sequence 2, Appli |
| 3 | 1268 | 100.0 | 247 | 2 | US-08-460-529B-10 | Sequence 10, Appl |
| 4 | 1268 | 100.0 | 247 | 2 | US-08-431-117A-2 | Sequence 2, Appli |
| 5 | 1268 | 100.0 | 247 | 4 | US-09-361-736B-10 | Sequence 10, Appl |
| 6 | 660.5 | 52.1 | 204 | 2 | US-08-208-005C-5 | Sequence 5, Appli |
| 7 | 660.5 | 52.1 | 204 | 2 | US-09-038-597A-5 | Sequence 5, Appli |
| 8 | 628 | 49.5 | 170 | 2 | US-08-460-529B-9 | Sequence 9, Appli |
| 9 | 628 | 49.5 | 170 | 4 | US-09-361-736B-9 | Sequence 9, Appli |
| 10 | 354.5 | 28.0 | 296 | 3 | US-08-831-132-14 | Sequence 14, Appl |

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| 11 | 354.5 | 28.0 | 296 | 3 | US-09-416-150-14 | Sequence 14, Appl |
| 12 | 354 | 27.9 | 302 | 3 | US-08-831-132-2 | Sequence 2, Appli |
| 13 | 354 | 27.9 | 302 | 3 | US-09-416-150-2 | Sequence 2, Appli |
| 14 | 354 | 27.9 | 302 | 4 | US-09-193-881-23 | Sequence 23, Appl |
| 15 | 354 | 27.9 | 302 | 4 | US-09-361-736B-12 | Sequence 12, Appl |
| 16 | 351.5 | 27.7 | 251 | 4 | US-09-361-736B-2 | Sequence 2, Appli |
| 17 | 333.5 | 26.3 | 251 | 2 | US-08-460-529B-2 | Sequence 2, Appli |
| 18 | 91 | 7.2 | 901 | 4 | US-09-828-062-8 | Sequence 8, Appli |
| 19 | 89.5 | 7.1 | 10182 | 3 | US-09-134-001C-3159 | Sequence 3159, Ap |
| 20 | 86 | 6.8 | 500 | 4 | US-09-198-452A-299 | Sequence 299, App |
| 21 | 85.5 | 6.7 | 311 | 4 | US-09-710-279-2460 | Sequence 2460, Ap |
| 22 | 85.5 | 6.7 | 656 | 3 | US-09-134-001C-4322 | Sequence 4322, Ap |
| 23 | 83.5 | 6.6 | 290 | 4 | US-09-655-908-6 | Sequence 6, Appli |
| 24 | 83.5 | 6.6 | 290 | 4 | US-09-655-908-8 | Sequence 8, Appli |
| 25 | 83.5 | 6.6 | 1027 | 4 | US-09-762-724-8 | Sequence 8, Appli |
| 26 | 83.5 | 6.6 | 1029 | 4 | US-09-762-724-6 | Sequence 6, Appli |
| 27 | 83 | 6.5 | 319 | 4 | US-09-710-279-792 | Sequence 792, App |
| 28 | 83 | 6.5 | 319 | 4 | US-09-710-279-2008 | Sequence 2008, Ap |
| 29 | 83 | 6.5 | 398 | 4 | US-09-710-279-44 | Sequence 44, Appl |
| 30 | 83 | 6.5 | 398 | 4 | US-09-710-279-1498 | Sequence 1498, Ap |
| 31 | 83 | 6.5 | 417 | 3 | US-09-134-001C-3810 | Sequence 3810, Ap |
| 32 | 82 | 6.5 | 362 | 3 | US-09-134-001C-4670 | Sequence 4670, Ap |
| 33 | 81 | 6.4 | 680 | 3 | US-09-298-924-4 | Sequence 4, Appli |
| 34 | 81 | 6.4 | 720 | 2 | US-08-840-236-1 | Sequence 1, Appli |
| 35 | 81 | 6.4 | 720 | 2 | US-08-505-448A-1 | Sequence 1, Appli |
| 36 | 79.5 | 6.3 | 609 | 4 | US-09-538-092-711 | Sequence 711, App |
| 37 | 79.5 | 6.3 | 708 | 1 | US-08-145-681-4 | Sequence 4, Appli |
| 38 | 79.5 | 6.3 | 708 | 1 | US-08-453-703-4 | Sequence 4, Appli |
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| 42 | 79.5 | 6.3 | 708 | 4 | US-09-633-739-4 | Sequence 4, Appli |
| 43 | 79 | 6.2 | 264 | 4 | US-09-134-000C-5831 | Sequence 5831, Ap |
| 44 | 78.5 | 6.2 | 1288 | 4 | US-09-546-934-4 | Sequence 4, Appli |
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ALIGNMENTS

RESULT 1

US-08-208-005C-2

; Sequence 2, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-2

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Query Match          100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    241 RTSHESA 247
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RESULT 2
US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:

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; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-2

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Query Match          100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy      241 RTSHESA 247
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Db      241 RTSHESA 247

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RESULT 3

US-08-460-529B-10

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; Sequence 10, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
;   APPLICANT: OLSEN, ET AL.
;   TITLE OF INVENTION: Human Stanniocalcin-alpha
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;     ADDRESSEE: CECCHI, STEWART & OLSTEIN
;     STREET: 6 BECKER FARM ROAD
;     CITY: ROSELAND
;     STATE: NEW JERSEY
;     COUNTRY: USA
;     ZIP: 07068
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5 INCH DISKETTE
;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/460,529B
;     FILING DATE: June 2, 1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US94/13206
;     FILING DATE: 10 NOV 1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MULLINS, J.G.
;     REGISTRATION NUMBER: 33,073
;     REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 201-994-1700
;     TELEFAX: 201-994-1744
;   INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:
;     .. LENGTH: 247 AMINO ACIDS
;     .. TYPE: AMINO ACID
;     .. STRANDEDNESS:
;     .. TOPOLOGY: LINEAR
;     MOLECULE TYPE: PROTEIN
US-08-460-529B-10

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Query Match          100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFORM 120
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Qy      121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180
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Db      121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180

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RESULT 4

US-08-431-117A-2

; Sequence 2, Application US/08431117A

; Patent No. 5994301

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,117A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/208,005

; FILING DATE: 8 MARCH 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-296

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
|||||

Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
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Db 241 RTSHESA 247

RESULT 5

US-09-361-736B-10

; Sequence 10, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120
 |||
 Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
 |||
 Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKvLLRNLRGEEDSPSHIK 240
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 Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKvLLRNLRGEEDSPSHIK 240

Qy 241 RTSHEsa 247
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 Db 241 RTSHEsa 247

RESULT 6

US-08-208-005C-5

; Sequence 5, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,005C

; FILING DATE: 8 MARCH 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-78

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 3.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

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Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECYCYS 130
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Qy 191 ASLFHILQTDHCAQ 204
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RESULT 7

US-09-038-597A-5

; Sequence 5, Application US/09038597A
; Patent No. 5877290

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:


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; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-5

```

```

Query Match          52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 3.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

```

```

Qy      11 LVISASATHEAEQNDVSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACLENSTCDTDGM 70
      ||:  :|| : :  :: |||::| : : : ::| |||| || |||| |||||
Db      12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy      71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECY 130
      :|||: | :|| | :||| |||||:||||| ||| |||||:|||||
Db      71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECY 130

Qy      131 KLNVC SI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRDSLMEKIGPNM 190
      :|::| :|: |||| ||||:| || ||||: |:||| |||:|: :| |: :|:|:|
Db      131 RLDICGVARSNPEAIGEVVQVPAHFNPYRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

Qy      191 ASLFHILQTDHCAQ 204
      :|| :|| || |
Db      191 ETLFQLLQNKHCPQ 204

```

RESULT 8

US-08-460-529B-9

```

; Sequence 9, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE

```

```

;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;      INFORMATION FOR SEQ ID NO:  9:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  170 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;      MOLECULE TYPE:  PROTEIN
US-08-460-529B-9

```

```

Query Match          49.5%;  Score 628;  DB 2;  Length 170;
Best Local Similarity  66.5%;  Pred. No. 1.3e-63;
Matches 113;  Conservative  30;  Mismatches  27;  Indels  0;  Gaps  0;

```

```

Qy      28  SPRKSRVAAQNSAEVVRCNLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ  87
      ||| :| :| : :|| |||| ||||| ||||:||||:||||:||||: |||||
Db      1  SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ  60

Qy      88  GKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECYSKLNVCSIAKRNPEAITE 147
      || ||||| |||||:||||| ||||:|:|:| ||||| ||||:|:|:| ||||: |
Db      61  GKTFFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy      148 VVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRDSLMEKIGPNMASLFHIL 197
      | |:|: | ||||: |:||| ||||| :| |: :| | | | :|
Db      121 VAQVPSQFPNRYYSTLLQSLLTCEDETVQVRAGLVSRLEPEMGVLFQLL 170

```

RESULT 9

US-09-361-736B-9

```

; Sequence 9, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 4; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.3e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
||| :| :| : :| |||| ||||| |||||:||||:||||:|:|:| |||||
Db 1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy 88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
|| |||||:||||| ||||:|:|:|:|||||:|:|:| ||||:|
Db 61 GKTFFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy 148 VVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRDSLMEKIGPNMASLFHIL 197
| |:|: | ||||: |:| ||||| :| |: :| | | :|
Db 121 VAQVPSQFPNRYYSTLLQSLLTCEDETVQVRAGLVSRLPEMGVLFQLL 170

RESULT 10

US-08-831-132-14

; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-831-132-14
```

```
Query Match          28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 5.9e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;
```

```
Qy      7 VLLVLVISASATHEAEQNDVSP-----RKSrvAAQNSAEVVRCLNSALQVGCGA 56
      | | | | : | : | | : | | : | | : | | : | | |
Db     10 VTLALVF--ATLDPAQGT DSTNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGV 67

Qy     57 FACLENSTCDTDGMYDICKSFLYSAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
      | | | | : | : | | : | | : | | : | | : | | : |
Db     68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy    117 FORMIAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVS 176
      : | : : | | | | : | | : | | : | : | : | | | |
Db    128 IREMFVQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy    177 TIRDSLMEKIGPNMASLFHIL-----QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
      : | : : : | | : | | : | | : | : | :
Db    188 AVTRSVQAQCEQSWGGLCSILSFCTSNIRPPTAAPEHQPLADRAQLSRPHHRDTHHLLT 247

Qy    225 LLRNLRGEDSPSHIK-----RTSHESA 247
      | : | | | | : | | : | |
Db    248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275
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RESULT 11

US-09-416-150-14

```
; Sequence 14, Application US/09416150
; Patent No. 6171822
```

GENERAL INFORMATION:

```
; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William
```

```
; TITLE OF INVENTION: STANNIOCALCIN-2
```

```
; NUMBER OF SEQUENCES: 22
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
```

```
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
```

```

;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/416,150
;      FILING DATE: 11-Oct-1999
;      CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/831,132
;      FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
;      NAME: Sawislak, Deborah A.
;      REGISTRATION NUMBER: 37,438
;      REFERENCE/DOCKET NUMBER: 96-01
;
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 206-442-6672
;      TELEFAX: 206-442-6678
;
; INFORMATION FOR SEQ ID NO: 14:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 296 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

```

```

Query Match          28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 5.9e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

```

```

Qy      7 VLLVLVISASATHEAEQNDVSP-----RKSrvAAQNSAEVVRCLNSALQVGC GA 56
      | | | | : | : | | : | | : | | : | | : | | |
Db      10 VTLALVF--ATLDPAQGTSTNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGC GV 67

Qy      57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCST 116
      | | | | : | : | | : | | : | | : | | : | | : |
Db      68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy      117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVS 176
      : | : : | | | | : | | : | | : : : | | | | |
Db      128 IREMVFQLQRECYLKHDLCsAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy      177 TIRDslMEKIGPNMASLFHIL-----QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
      : | : : : | | : | | : | | : | | : | :
Db      188 AVTRSVQAQCEQSWGGLCSILSFCTSNiQRPPTAAPEHQPLADRAQLSRPHHRDTHHILT 247

Qy      225 LLRNLRGEEDSPSHIK-----RTSHESA 247
      | : | | | | | | : | |
Db      248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275

```

RESULT 12

US-08-831-132-2

```

; Sequence 2, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.

```

```

; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-831-132-2

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Qy 223 KVLLRNLRGEEDSPSH 238
: | :|| | ||
Db 252 RETGRGAKGERGSKSH 267

RESULT 13

US-09-416-150-2

; Sequence 2, Application US/09416150

; Patent No. 6171822

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William

; TITLE OF INVENTION: STANNIOCALCIN-2

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-416-150-2

Query Match 27.9%; Score 354; DB 3; Length 302;

Best Local Similarity 32.4%; Pred. No. 6.9e-32;

Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60

: | :| | |
Db 252 RETGRGAKGERGSKSH 267

Search completed: January 14, 2005, 22:22:14
Job time : 46 secs

OM protein - protein search, using sw model

Run on: January 14, 2005, 22:04:00 ; Search time 40 Seconds
(without alignments)
594.139 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | Length | DB | ID | Description |
|------------|-------|---------|--|--------|----|--------|--------------------|
| | | Match | | | | | |
| 1 | 680.5 | 53.7 | | 263 | 2 | A54648 | stanniocalcin prec |
| 2 | 662.5 | 52.2 | | 256 | 2 | I51197 | stanniocalcin - co |
| 3 | 354 | 27.9 | | 302 | 2 | JE0357 | stanniocalcin homo |
| 4 | 150 | 11.8 | | 40 | 2 | B60841 | teleocalcin - coho |
| 5 | 149 | 11.8 | | 40 | 2 | A60841 | teleocalcin - sock |
| 6 | 123 | 9.7 | | 33 | 2 | S06337 | teleocalcin - rain |
| 7 | 102 | 8.0 | | 473 | 2 | T04799 | hypothetical prote |
| 8 | 94 | 7.4 | | 1105 | 2 | T18295 | Ap-3 adaptor compl |
| 9 | 90.5 | 7.1 | | 289 | 2 | T50776 | hypothetical prote |
| 10 | 90.5 | 7.1 | | 783 | 2 | T38690 | probable regulator |
| 11 | 89.5 | 7.1 | | 1126 | 2 | T01491 | ubiquitin-protein |
| 12 | 89 | 7.0 | | 305 | 2 | T08121 | peroxidase (EC 1.1 |
| 13 | 88 | 6.9 | | 473 | 2 | T45954 | hypothetical prote |

| | | | | | | |
|----|------|-----|------|---|--------|--------------------|
| 14 | 87.5 | 6.9 | 1465 | 2 | S45628 | DNA-directed DNA p |
| 15 | 86 | 6.8 | 470 | 2 | F86526 | Mg++ transporter [|
| 16 | 86 | 6.8 | 470 | 2 | H72097 | mg++ transporter (|
| 17 | 86 | 6.8 | 510 | 2 | T45952 | hypothetical prote |
| 18 | 86 | 6.8 | 556 | 2 | S51858 | probable membrane |
| 19 | 86 | 6.8 | 581 | 2 | S58201 | probable membrane |
| 20 | 83 | 6.5 | 250 | 2 | D69215 | conserved hypothet |
| 21 | 83 | 6.5 | 250 | 2 | S30584 | hypothetical prote |
| 22 | 83 | 6.5 | 365 | 2 | T06693 | hypothetical prote |
| 23 | 83 | 6.5 | 1093 | 2 | T50652 | AP-3 complex beta3 |
| 24 | 83 | 6.5 | 1094 | 2 | T50651 | AP3-complex beta-3 |
| 25 | 82.5 | 6.5 | 869 | 2 | A88710 | protein C43G2.2 [i |
| 26 | 82.5 | 6.5 | 1483 | 2 | S30015 | hypothetical prote |
| 27 | 82.5 | 6.5 | 1757 | 2 | T05204 | hypothetical prote |
| 28 | 82.5 | 6.5 | 2335 | 2 | T40186 | probable phosphati |
| 29 | 82.5 | 6.5 | 2535 | 2 | T04824 | hypothetical prote |
| 30 | 82 | 6.5 | 815 | 2 | G72209 | conserved hypothet |
| 31 | 82 | 6.5 | 925 | 2 | T01384 | hypothetical prote |
| 32 | 81.5 | 6.4 | 463 | 2 | T15416 | hypothetical prote |
| 33 | 81.5 | 6.4 | 549 | 2 | F64640 | conserved hypothet |
| 34 | 81.5 | 6.4 | 708 | 1 | TFBOL | lactotransferrin p |
| 35 | 81 | 6.4 | 358 | 2 | S76692 | hypothetical prote |
| 36 | 81 | 6.4 | 720 | 2 | JC5131 | glycosyltransferas |
| 37 | 81 | 6.4 | 1375 | 2 | T18961 | FAB1 protein homol |
| 38 | 81 | 6.4 | 4377 | 2 | A55575 | ankyrin 3, long sp |
| 39 | 80 | 6.3 | 281 | 2 | H84720 | probable endonucle |
| 40 | 80 | 6.3 | 509 | 1 | VGNVPC | major envelope gly |
| 41 | 80 | 6.3 | 509 | 2 | T10395 | protein gp64 - Org |
| 42 | 80 | 6.3 | 985 | 2 | T00633 | Ca2+-transporting |
| 43 | 80 | 6.3 | 998 | 2 | T52581 | Ca2+-transporting |
| 44 | 80 | 6.3 | 1178 | 2 | S54073 | probable membrane |
| 45 | 80 | 6.3 | 1188 | 2 | T46608 | zinc finger protei |

ALIGNMENTS

RESULT 1

A54648

stanniocalcin precursor - Australian eel

N;Alternate names: Stannius corpuscle secretory protein

C;Species: *Anguilla australis* (Australian eel)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: A54648

R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.;

Ryan, G.B.; Trahair, J.F.; Tregear, G.W.; Coghlan, J.P.

Mol. Cell. Endocrinol. 54, 123-133, 1987

A;Title: Purification and cloning of a corpuscles of Stannius protein from *Anguilla australis*.

A;Reference number: A54648; MUID:88083961; PMID:3319739

A;Accession: A54648

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-263 <BUT>

A;Cross-references: UNIPROT:P18301

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-263/Product: stanniocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;
Best Local Similarity 61.4%; Pred. No. 3.7e-51;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

```
Qy      1 MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL 60
      ||: | ::| ||:  :| :| :::: :||| :| :| : ::| |||| ||||| |||||
Db      1 MLRMSG LILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120
      :|||:| |||:| :|:| | | | | | | | | | | | | | | | | | | | | | | |
Db      60 DNSTCNTDGMHEICRSFLHGA AKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy      121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD 180
      |:| | | | | | | | | :|:|:| | | | :| | | :| | | :| :| | | | | :|
Db      120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCEDETV EQVRA 179

Qy      181 SLMEKIGPNMASLFHILQTDHC 202
      |: :: | | | | :||| |
Db      180 GLVSRLEPEMGVLFQLLQTKAC 201
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RESULT 2

I51197

stanniocalcin - coho salmon

C;Species: Oncorhynchus kisutch (coho salmon)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I51197

R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.

Mol. Cell. Endocrinol. 90, 7-15, 1992

A;Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.

A;Reference number: I51197; MUID:93246046; PMID:1363790

A;Accession: I51197

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-256 <WAG>

A;Cross-references: UNIPROT:Q08264; GB:S59519; NID:g299926; PIDN:AAB26419.1; PID:g299927

Query Match 52.2%; Score 662.5; DB 2; Length 256;
Best Local Similarity 53.4%; Pred. No. 1.3e-49;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

```
Qy      11 LVISASATHEAEQNDVSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACLENSTCDTDGM 70
      ||:  :|| : :  :..|||:| :| : : ::| |||| | | |||| ||||| |||||
Db      12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy      71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRMIAEVQEECY 130
      :|||: | :|| | :||| | | | | :| | | | | | | | | | | | | | | |
Db      71 HDICQLFFHTAATFNTQGKTFVKESLR CIANGVT SKVFQTIRRCGVFQRMISEVQEECY 130

Qy      131 KLVNCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRDSLMEKIGPNM 190
      :|:| | :|: | | | | | | | | | | | | | | :| :| :| :| :| :| :| :|
Db      131 RLDICGVARSNPEAIGEVVQVPAHF PNRYYSTLLQSL LACDEETVAVVRAGLVARLGPD 190

Qy      191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLRLNLRGEEDSPSHI 239
```


R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
 Gen. Comp. Endocrinol. 72, 237-246, 1988
 A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.
 A;Reference number: A60841; MUID:89065334; PMID:3197944
 A;Accession: B60841
 A;Molecule type: protein
 A;Residues: 1-40 <WAG>
 A;Cross-references: UNIPROT:Q08264
 C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim uptake through the gills.
 C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 150; DB 2; Length 40;
 Best Local Similarity 66.7%; Pred. No. 2e-06;
 Matches 26; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 35 AAQNSAEVVRLNSALQVGCGAFACLENSTCDTDGMYDI 73
 :: : ::| |||| || |||| ||||| |||||:|
 Db 2 SSNSPSDVARCLNGALAVGCGTFACLEXSTCDTDGMHDI 40

RESULT 5

A60841
 teleocalcin - sockeye salmon (fragment)
 C;Species: Oncorhynchus nerka (sockeye salmon)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: A60841
 R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
 Gen. Comp. Endocrinol. 72, 237-246, 1988
 A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.
 A;Reference number: A60841; MUID:89065334; PMID:3197944
 A;Accession: A60841
 A;Molecule type: protein
 A;Residues: 1-40 <WAG>
 A;Cross-references: UNIPROT:P43649
 C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim uptake through the gills.
 C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 149; DB 2; Length 40;
 Best Local Similarity 76.5%; Pred. No. 2.4e-06;
 Matches 26; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 40 AEVVRLNSALQVGCGAFACLENSTCDTDGMYDI 73
 ::| |||| || |||| ||||| |||||:|
 Db 7 SDVARCLNGALDVGCGTFACLEXSTCDTDGMHDI 40

RESULT 6

S06337
 teleocalcin - rainbow trout (fragment)
 N;Alternate names: hypocalcin
 C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
 C;Accession: S06337
 R;Lafeber, F.P.J.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Flik, G.; Herrmann-Erlee, M.P.M.; Pang, P.K.T.; Wendelaar Bonga, S.E.
 Gen. Comp. Endocrinol. 69, 19-30, 1988
 A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius corpuscles.
 A;Reference number: S06337; MUID:88196801; PMID:3360288
 A;Accession: S06337
 A;Molecule type: protein
 A;Residues: 1-33 <LAF>
 A;Note: 7-Glu was also found
 C;Keywords: dimer; glycoprotein; hormone
 F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.7%; Score 123; DB 2; Length 33;
 Best Local Similarity 65.6%; Pred. No. 0.00033;
 Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 35 AAQNSAEVVRCLNSALQVCGAFACLENSTCD 66
 :: : ::| |||| || |||| |||||
 Db 2 SSNSPSDVARCLNGALAVGCGTFACLENSTCD 33

RESULT 7

T04799

hypothetical protein F10M23.100 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04799

R;Bevan, M.; Lecharny, A.; Chedfor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.

submitted to the Protein Sequence Database, February 1999

A;Reference number: Z15385

A;Accession: T04799

A;Molecule type: DNA

A;Residues: 1-473 <BEV>

A;Cross-references: UNIPROT:Q9SZ16; EMBL:AL035440

A;Experimental source: cultivar Columbia; BAC clone F10M23

C;Genetics:

A;Map position: 4

A;Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3

A;Note: F10M23.100

Query Match 8.0%; Score 102; DB 2; Length 473;
 Best Local Similarity 21.0%; Pred. No. 0.5;
 Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

Qy 26 SVSPRKSRVAAQNSAEVVRCLNSALQVCGAFACLENSTCDT----DGM YDICKSF-LYS 80
 :| :| :||: ||:: |: | :| | | || | :
 Db 50 NVYKKKVELAAKSRAELLQTLSD-----ATVELSNLTTALGEKSYIDICDSMSLFP 100
 Qy 81 AAKFDTQGKAFVKESLKCIA-----NG-- 102
 | | :| | || |
 Db 101 LQPDKTS GT--IKEQLSAIAPALEQLWQQKEERVRAFSDVQSQIQKICEEIAGGLNNGPH 158
 Qy 103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----NVCSIAKRN-PEAITEV-- 148


```

      | : |::| ||| : |::| :|          ::||: : : : |||
Db      159 VVDETDLSLKRLDDFQRKLQELQKEKSDRLQKVLEFVSTVHDLCAVLRDLDFLSTVTEVHP 218

Qy      149 -----VQLPNHFSNRYNRLVRSLLCEDTVSTIRDSLMEKIGPNMASLFHILQT 199
      || : || || ::| || : :: ::: : |:::|
Db      219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQLKK--LQELATQLTDLWNLMMDT 273

```

RESULT 8

T18295

Ap-3 adaptor complex beta3A chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18295

R;Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusiniak, M.E.; Eicher, E.M.; Robinson, M.S.; Gorin, M.B.; Swank, R.T. Hum. Mol. Genet. 8, 323-330, 1999

A;Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the mouse hypopigmentation mutant pearl, a model for Hermansky-Pudlak syndrome and night blindness.

A;Reference number: Z18864; MUID:99135912; PMID:9931340

A;Accession: T18295

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1105 <FEN>

A;Cross-references: UNIPROT:Q9Z1T1; EMBL:AF103809; NID:g3885987; PID:g3885988; PIDN:AAC78338.1

A;Experimental source: strain C3H/HeJ

C;Genetics:

A;Gene: Ap3b1

A;Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;

Best Local Similarity 21.2%; Pred. No. 6.7;

Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

```

Qy      1 MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60
      :||:  :|: :: |          :||:  | | :|| | | :|          :
Db      308 LLQSRNAAVVMAVAQLYWH-----ISPKSE--AGVISKSLVRLLSNREVQYIVLQNI 358

Qy      61 ENSTCDTDGMYD-ICKSFLYSAKFDTQGKAFVKESLKCIANGVT SKVFL----- 109
      : : ||:: ||| | : | | | | | :|| |
Db      359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy      110 -----AIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNP EAIT E---VVQLPNHFS 156
      | ||:|  |:| | |:: | || :: |: : |  |::
Db      418 DKQFAAATIQTIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIKLLQMQ 473

Qy      157 NRYNRLVRSLL E-CD EDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNR RR 215
      : ::| : : | || | |:: || | | : |
Db      474 PAQHGEIIRHMAKFLDSITVPVARASILW LIGEN-----CERV PKIA----- 515

Qy      216 TNEPQKLKVLLRNLRGEED 234
      | |: : :: | :|
Db      516 ---PDVLRKMAKSFTSEDD 531

```

RESULT 9

T50776

hypothetical protein [imported] - Vitis vinifera

C;Species: Vitis vinifera

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C;Accession: T50776

R;Matsumoto, S.; Dry, I.B.; Thomas, M.

DNA Seq. 8, 109-112, 1997

A;Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.

A;Reference number: Z25233

A;Accession: T50776

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-289 <MAT>

A;Cross-references: UNIPROT:P93798; EMBL:AB001375; PIDN:BAA19246.1

A;Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;

Best Local Similarity 19.9%; Pred. No. 2.7;

Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

```

Qy      8 LLVLVISASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACLENSTCDT 67
      |  :: | : : || |  : :      : : | : || |  | : | : | :
Db      59 LSTVIQSSDSKHEAAQ--AYADAGHCYKkTSAKEAISCLEQA-----AYFLDNGRfNM 110

Qy      68 DG-----MYDICKSFLYsAAKFDTQGKAfVKESLKCIAngVTSKVFLAIRRCSTfQR 119
      |      :| :: ::|  :  | :      : |      ||  :||  :  :| :
Db      111 AGKYyKEIAELYELEQNFEQAIiYFEKAADIYQSEEAiTaanQCNAKVAQFAAQLEQYQK 170

Qy      120 MIAEVQEECYSKLN-----VCsIAKRNPeAITEVVQL-----PNHfSNR 158
      |  ::      ||      :| : | : |||  :      |      |
Db      171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPtFSGTR 230

Qy      159 YYNRLVRSLLCEDEDTVSTIRDSLME 184
      | ||      ||: |  | :: |
Db      231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256

```

RESULT 10

T38690

probable regulatory protein - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004

C;Accession: T38690

R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21805

A;Accession: T38690

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-783 <BRO>

A;Cross-references: UNIPROT:O14130; EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066;

SPDB:SPAC3C7.04

A;Experimental source: strain 972h-; cosmid c3C7

C;Genetics:

A;Gene: SPDB:SPAC3C7.04

A;Map position: 1
C;Superfamily: GAL4 zinc binuclear cluster homology
F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

```
Query Match          7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 9;
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

Qy      10 VLVISASATHEAEQNDSVSPRKSRV-----AAQNSAEVVRCLNSALQVGCGAF----- 57
      ::::|      :|   |||  |:      ||::  :|  | :  |:  | :|
Db      535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDNYNT 594

Qy      58 -----ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI----- 99
      |:      |: |   ||   : |||  :  :|   |   : |
Db      595 FSSALVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy      100 ----ANGVTSKV-FLAIRRCSTFORMIAEVQ-----EECYSKLNVCSIAKRNPETAITEVV 149
      || ||:  |:|      :|| ||||      |:  |  |   ||  ::|
Db      651 ARSDGNGNTSQSGFMA-----WQRWIAEVSADPEPEKLMSPYNKSIIGGRNSNSLTTPNA 704

Qy      150 QLPNHFSNRYYNR-----LVRSLLECEDTSTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
      |   |  ::      |  | |: | :  ::  | :  |  |::|  || :  ||
Db      705 NLGADVS--FFPTDDTSFLLDHSKLDLDDLEKFASTLDPI--KTTPLANDSSLLNWANTD 760
```

RESULT 11

T01491

ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01491

R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, J.; Araujo, R.; Au, M.; Brendel, V.; Buehler, E.; Conway, A.B.; Conway, A.R.; Dewar, K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.; Theologis, A.
submitted to the EMBL Data Library, June 1998

A;Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.

A;Reference number: Z14334

A;Accession: T01491

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1126 <VYS>

A;Cross-references: UNIPROT:O64605; EMBL:AC003671; NID:g2833627; PID:g3176690;
GSPDB:GN00059; ATSP:F1707.15

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: ATSP:F1707.15

A;Map position: 1

A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3;
1093/2

F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

```
Query Match          7.1%; Score 89.5; DB 2; Length 1126;
Best Local Similarity 22.1%; Pred. No. 17;
Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

Qy      14 SASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCD----- 66
```

```

      | :      : ||      || : ||      | || :      | || :      : : | :
Db      412 SSETQKDAESELVARRK-----NCAEL---YNIFLQLP-----QSDLCNLCMLLGY 455
Qy      67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
      : | : | :      | | | : | : | : | : | : | : | : | : | : | :
Db      456 EGLSDKIYSLAGEVLKKLAADVTHRKFFTKELSELASGLSSSTVRVLATLSTTQKM--- 512
Qy      124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIR----- 179
      | || : |      : | | : : : : : : | : | | : : : :
Db      513 -----SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 562
Qy      180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
      : | : : | : :      || || | |
Db      563 ALEPLWQELGQCIS--MTELQLDHTAAT 588

```

RESULT 12

T08121

peroxidase (EC 1.11.1.7) - flax (fragment)

C;Species: Linum usitatissimum (flax)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C;Accession: T08121

R;Omann, F.; Tyson, H.

submitted to the EMBL Data Library, February 1998

A;Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.

A;Reference number: Z16366

A;Accession: T08121

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-305 <OMA>

A;Cross-references: UNIPROT:O65029; EMBL:AF049881; NID:g2944416;

PIDN:AAC05277.1; PID:g2944417

A;Experimental source: cv. Stormont Cirrus

C;Genetics:

A;Gene: PER4

C;Superfamily: peroxidase

C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase

F;23-103/Disulfide bonds: #status predicted

F;50/Active site: Arg #status predicted

F;54,181/Binding site: heme iron (His) (axial ligands) #status predicted

F;56-61/Disulfide bonds: #status predicted

F;109-301/Disulfide bonds: #status predicted

F;188-213/Disulfide bonds: #status predicted

Query Match 7.0%; Score 89; DB 2; Length 305;

Best Local Similarity 21.9%; Pred. No. 3.9;

Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

```

Qy      11 LVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRC LNSALQVGCGA-FACLE-NSTCDTD 68
      | : : ||      | : |      : : |      : : : : | | : | : : |
Db      65 LLLDDTATFTGEKN--AGPNQNSV---RGFDIIDTIKTRVEAACNATVSCADILALAARD 119
Qy      69 GMYDI-----CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
      | : :      : : ||      || | | | : | |
Db      120 GVVLVGGPTWTVP LGRRDARTASQSAANAQIPAPG---SSLGTITNLF TNKGLTARDVTI 176
Qy      111 -----IRRCSTFQRMIAEVQEECYSKLNV-----CSIAKRN-PEA-----ITEVVQLP 152

```

```

      ||::||: |      |: |:      : : | |:|      : : |
Db      177 LSGAHTIGQARCTTFRQRI-----YNDTNIDPAFATTRRGNC PQAGAGANLAPLDGTP 229
Qy      153 NHFSNRYYNRLV--RSLLECEDTVST-IRDSLMEKIGPNMASLFHILQTDHCAQ----- 204
      | ||| | | | | | | |:: : : |:|: | |: | | |
Db      230 TQFDNRYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT----FATDFAAAMVRMG 285
Qy      205 -----THPRADFNRRRTN 217
      |: | | | |
Db      286 NISPLTGTNGEIRFNCRRPN 305

```

RESULT 13

T45954

hypothetical protein F7J8.120 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45954

R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z23018

A;Accession: T45954

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-473 <BEV>

A;Cross-references: UNIPROT:Q9LFC2; EMBL:AL137189

A;Experimental source: cultivar Columbia; BAC clone F7J8

C;Genetics:

A;Map position: 5

A;Introns: 29/1; 428/3

A;Note: F7J8.120

C;Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;

Best Local Similarity 22.6%; Pred. No. 8.1;

Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

```

Qy      27 VSPRKS RVAQNSAEVVRCLNSALQVGC GAFACLEN---STCD---TDGMYDICKS-FLY 79
      : |::| : :|| | : || | | | | | | | | |
Db      16 IDEEKNKVVLAEAGTIVRL LAKHRKSDPVTIGCLRNLYTSV VDMELDDFETDACKQMLLY 75
Qy      80 SAAKFDTQ GKAF-----VKESLKCIANGVTSKVFLAIRRCSTFQRMIAE-----VQEEC-- 128
      : | : | |||| : | | | | : : : |
Db      76 PKNIREAQYRNFKLNIDTNESLKCFG----CRFFSICRMCSNFNTSLCKCGKLMNEEISF 131
Qy      129 --YSKLNVC SIAKRNPEA--ITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD SLME 184
      | : : | : | : ||: ::| : : : |::| : || :|: ::
Db      132 LEYEENDVEGVFMRDKSSFIIITDDLRLTDDST----SLLQTLKDLGCADVSKLREQVLD 187
Qy      185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLRLNLRGEEDSPSHI 239
      || | : : | | | | : : |:: | : :|: | :
Db      188 -IG-----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV 240

```

RESULT 14

S45628

DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse
 N;Alternate names: DNA polymerase alpha/DNA primase complex 180K chain
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S45628; A46642
 R;Stadlbauer, F.; Brueckner, A.; Rehfuess, C.; Eckerskorn, C.; Lottspeich, F.;
 Foerster, V.; Tseng, B.Y.; Nasheuer, H.P.
 Eur. J. Biochem. 222, 781-793, 1994
 A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
 A;Reference number: S45628; MUID:94298818; PMID:8026492
 A;Accession: S45628
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1465 <STA>
 A;Cross-references: UNIPROT:P33609; EMBL:D17384; NID:g397829; PIDN:BAA04202.1;
 PID:g442471
 R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka,
 F.
 J. Biol. Chem. 268, 8111-8122, 1993
 A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA
 polymerase alpha-primase complex and their gene expression during cell
 proliferation and the cell cycle.
 A;Reference number: A46642; MUID:93216788; PMID:8463324
 A;Accession: A46642
 A;Status: preliminary.
 A;Molecule type: mRNA; protein
 A;Residues: 4-1465 <MIY>
 A;Experimental source: FM3A cells
 A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIP:129147)
 C;Superfamily: DNA polymerase
 C;Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;
 Best Local Similarity 20.7%; Pred. No. 34;
 Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

Qy 6 AVLLVLVISASAT-----HEAEQNDSVSPRKS RVAAQNSAEVVRLNSALQVGC GAFA 58
 |||: | : :| | : |||: : : : | |
 Db 1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----DCEKFK 1284
 Qy 59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT-----SKVFLAIR 112
 || | | | : :|| : : | : : : : | : : | : : ||
 Db 1285 CLCPS-CGTENIYD----NVFEGSGLDMEPSLYRCSNV DCKVSPLTFMVQLSNKLIMDIR 1339
 Qy 113 RCSTFQRMIAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFS 156
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 Db 1340 RCI-----KYYDGWLIC----EEPTCCSRLRRLPLHFS 1369

RESULT 15

F86526

Mg++ transporter [imported] - Chlamydomophila pneumoniae (strain J138)
 C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F86526
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;
 Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: F86526

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-470 <STO>

A;Cross-references: UNIPROT:Q9Z8Q2; GB:BA000008; NID:g8978660; PIDN:BAA98496.1; GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: mgtE

C;Superfamily: magnesium transport protein mgtE

Query Match 6.8%; Score 86; DB 2; Length 470;

Best Local Similarity 22.9%; Pred. No. 12;

Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

Qy 56 AFACLENSTCDDT-GMYDICK-----SFLYSAKFDTQGKAFVKESLKCIANGVTSK 106

|| || || :|: | | : : : : | : : | || |:

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Qy 107 VFLAIR-----RCSTFORMIAEVQEECYSKLNVCSIAKRNP--EAITEVVQLPNHFSNRY 159

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Qy 160 YNRLVRSLLCEDTSTVSTIRDSLMEKIGPNMA-----SLFHIL-----QTDHCAQTHP 207

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Db 172 GIDLTR-----LVFVLDFKGE 187

Search completed: January 14, 2005, 22:21:27

Job time : 52 secs

OM protein - protein search, using sw model

Run on: January 14, 2005, 22:18:31 ; Search time 149 Seconds
(without alignments)
598.916 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------------------|-------------------|
| 1 | 1268 | 100.0 | 247 | 9 | US-09-840-989A-2 | Sequence 2, Appli |
| 2 | 1268 | 100.0 | 247 | 9 | US-09-361-736-10 | Sequence 10, Appl |
| 3 | 1268 | 100.0 | 247 | 13 | US-10-116-051-2 | Sequence 2, Appli |
| 4 | 1268 | 100.0 | 247 | 14 | US-10-177-293-441 | Sequence 441, App |
| 5 | 1268 | 100.0 | 247 | 14 | US-10-418-226-10 | Sequence 10, Appl |
| 6 | 1268 | 100.0 | 247 | 14 | US-10-465-572-18 | Sequence 18, Appl |
| 7 | 1268 | 100.0 | 247 | 15 | US-10-372-683-41 | Sequence 41, Appl |
| 8 | 1268 | 100.0 | 247 | 17 | US-10-614-990-2 | Sequence 2, Appli |
| 9 | 1268 | 100.0 | 247 | 17 | US-10-723-860-4202 | Sequence 4202, Ap |
| 10 | 937 | 73.9 | 276 | 9 | US-09-925-300-1426 | Sequence 1426, Ap |
| 11 | 662.5 | 52.2 | 256 | 9 | US-09-840-989A-3 | Sequence 3, Appli |
| 12 | 662.5 | 52.2 | 256 | 17 | US-10-614-990-3 | Sequence 3, Appli |
| 13 | 660.5 | 52.1 | 204 | 13 | US-10-116-051-10 | Sequence 10, Appl |
| 14 | 628 | 49.5 | 170 | 9 | US-09-361-736-9 | Sequence 9, Appli |
| 15 | 628 | 49.5 | 170 | 14 | US-10-418-226-9 | Sequence 9, Appli |
| 16 | 358 | 28.2 | 70 | 9 | US-09-864-761-37770 | Sequence 37770, A |
| 17 | 354 | 27.9 | 302 | 9 | US-09-193-881-23 | Sequence 23, Appl |
| 18 | 354 | 27.9 | 302 | 14 | US-10-177-293-443 | Sequence 443, App |
| 19 | 354 | 27.9 | 302 | 14 | US-10-338-395-23 | Sequence 23, Appl |
| 20 | 354 | 27.9 | 302 | 14 | US-10-418-226-12 | Sequence 12, Appl |
| 21 | 354 | 27.9 | 302 | 14 | US-10-364-889-4 | Sequence 4, Appli |
| 22 | 354 | 27.9 | 302 | 14 | US-10-295-027-100 | Sequence 100, App |
| 23 | 354 | 27.9 | 302 | 15 | US-10-173-999-80 | Sequence 80, Appl |
| 24 | 354 | 27.9 | 302 | 15 | US-10-058-270A-22 | Sequence 22, Appl |
| 25 | 354 | 27.9 | 302 | 17 | US-10-789-378-74 | Sequence 74, Appl |
| 26 | 351.5 | 27.7 | 251 | 14 | US-10-418-226-2 | Sequence 2, Appli |
| 27 | 333.5 | 26.3 | 251 | 9 | US-09-361-736-2 | Sequence 2, Appli |
| 28 | 303 | 23.9 | 118 | 13 | US-10-116-051-9 | Sequence 9, Appli |
| 29 | 95.5 | 7.5 | 299 | 15 | US-10-282-122A-49895 | Sequence 49895, A |
| 30 | 94.5 | 7.5 | 415 | 17 | US-10-425-115-320042 | Sequence 320042, |
| 31 | 92 | 7.3 | 1010 | 17 | US-10-425-115-312927 | Sequence 312927, |
| 32 | 91 | 7.2 | 901 | 10 | US-09-828-062-8 | Sequence 8, Appli |
| 33 | 91 | 7.2 | 901 | 16 | US-10-768-511-8 | Sequence 8, Appli |
| 34 | 90.5 | 7.1 | 783 | 15 | US-10-149-310-96 | Sequence 96, Appl |
| 35 | 90 | 7.1 | 281 | 11 | US-09-973-278-172 | Sequence 172, App |
| 36 | 90 | 7.1 | 281 | 11 | US-09-973-278-277 | Sequence 277, App |
| 37 | 90 | 7.1 | 331 | 15 | US-10-264-049-2324 | Sequence 2324, Ap |
| 38 | 89.5 | 7.1 | 622 | 16 | US-10-437-963-161551 | Sequence 161551, |
| 39 | 89.5 | 7.1 | 1123 | 15 | US-10-282-122A-70581 | Sequence 70581, A |
| 40 | 89.5 | 7.1 | 10203 | 16 | US-10-661-809-23 | Sequence 23, Appl |
| 41 | 89 | 7.0 | 201 | 17 | US-10-425-115-320050 | Sequence 320050, |
| 42 | 89 | 7.0 | 431 | 17 | US-10-425-115-285165 | Sequence 285165, |
| 43 | 86 | 6.8 | 401 | 15 | US-10-425-114-63193 | Sequence 63193, A |
| 44 | 86 | 6.8 | 470 | 15 | US-10-282-122A-54827 | Sequence 54827, A |
| 45 | 86 | 6.8 | 500 | 15 | US-10-289-762-299 | Sequence 299, App |

ALIGNMENTS

RESULT 1

US-09-840-989A-2

; Sequence 2, Application US/09840989A

; Patent No. US20020042372A1

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; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2
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Query Match          100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTskVFLAIRRCSTFQRM 120

Qy      121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180

Qy      181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKvLLRNLRGEEDSPSHIK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      241 RTSHESA 247
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Db      241 RTSHESA 247
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RESULT 2

US-09-361-736-10

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; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
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; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-10

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Query Match          100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
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Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy    241 RTS HESA 247
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Db    241 RTS HESA 247

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RESULT 3

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; Sequence 2, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | MLQNSAVLLVLVISASATHEAEQND SVSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL | 60 |
| Qy | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM | 120 |
| | | | |
| Db | 61 | ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM | 120 |
| Qy | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECDEDTVSTIRD | 180 |
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| Db | 121 | IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECDEDTVSTIRD | 180 |
| Qy | 181 | SIMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK | 240 |
| | | | |
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| Db | 241 | RTSHESA 247 | |

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; Sequence 441, Application US/10177293
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; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula

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; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pustai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-441
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Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Qy    121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD 180
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Db    121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
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Qy      241 RTSHESA 247
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Db      241 RTSHESA 247

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US-10-418-226-10

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; Publication No. US20030181663A1
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; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-10-418-226-10

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Query Match          100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60
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Db      1 MLQNSAVLLVLVISASATHEAEQNDVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60

Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120
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Db      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120

Qy      121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180

Qy      181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy      241 RTSHESA 247
          |||||||
Db      241 RTSHESA 247

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US-10-465-572-18

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Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRC LNSALQVGCGAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
      |||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDETVSTIRD 180
      |||
Db    121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDETVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
      |||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy    241 RTSHESA 247
      |||
Db    241 RTSHESA 247

```

US-10-372-683-41

```
; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT:  PEALE JR., FRANKLIN V.
; APPLICANT:  WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
```

; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFQRM 120

Qy    121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRS LLECEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRN LRGEEDSPSHIK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRN LRGEEDSPSHIK 240

Qy    241 RTSHESA 247
          |||||
Db    241 RTSHESA 247
```

RESULT 8

US-10-614-990-2

; Sequence 2, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL 60
|||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
|||||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
|||||

Db 121 IAEVQEECYSKLNVCSI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTS HESA 247
|||||

Db 241 RTS HESA 247

RESULT 9

US-10-723-860-4202

; Sequence 4202, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
&

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NPUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4202

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-723-860-4202

Query Match 100.0%; Score 1268; DB 17; Length 247;

Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLQNSAVLLVLVISASATHEAEQNDSPRKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLQNSAVLLVLVISASATHEAEQNDSPRKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60

Qy     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFORM 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT SKVFLAIRRCSTFORM 120

Qy    121 IAEVQEECYSKLNVCSI AKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 IAEVQEECYSKLNVCSI AKRNPEAITEVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD 180

Qy    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Qy    241 RTSHESA 247
        |||||||
Db    241 RTSHESA 247
```

RESULT 10

US-09-925-300-1426

; Sequence 1426, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1426

; LENGTH: 276

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (43)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (273)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (275)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;
Best Local Similarity 99.5%; Pred. No. 6.8e-87;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MLQNSAVLLVLVISASATHEAEQNDSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACL 60
          |||
Db      89 MLQNSAVLLVLVISASATHEAEQNDSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACL 148

Qy      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
          |||
Db     149 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 208

Qy     121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 180
          |||
Db     209 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRD 268

Qy     181 SLMEKI 186
          |||
Db     269 SLMEXI 274
```

RESULT 11

US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 9; Length 256;
Best Local Similarity 53.4%; Pred. No. 6.1e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

```
Qy      11 LVISASATHEAEQNDSPRKSrvAAQNSAEVVRCLNSALQVGCgAFACLENSTCDTDGM 70
          ||: :|| : : :: ||::|| :: : ::| |||| || |||| |||
Db      12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy      71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECY 130
          :||: | :|| | :||| ||||:||||||| ||| ||||:|||||||
Db      71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECY 130

Qy     131 KLVNCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECEDTVSTIRDSLMEKIGPNM 190
```

```

          :|::| :|: |||| |::| | | ||:: |::|| |::||: :| |: :|::|
Db      131 RLDICGVARSNPEAIGEVVQVPAHFNPYRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

Qy      191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLRLNLRGEEDSPSHI 239
          :||:| | | : : | | | : :|| : |::
Db      191 ETLFQLLQNKHCPQGSNQGPNAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

```

RESULT 12

US-10-614-990-3

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; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3

```

```

Query Match          52.2%; Score 662.5; DB 17; Length 256;
Best Local Similarity 53.4%; Pred. No. 6.1e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

```

```

Qy      11 LVISASATHEAEQNDVSPRKS RVAAQNSAEVVRLNSALQVGC GAFACLENSTCDTDGM 70
          ||: :| : : :: ||::| : : : ::| ||| | | ||| |||||
Db      12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy      71 YDICKSFLYSAAKFDTQGKAFVKESLKC IANGVTSKVFLAIRRCSTFORMIAEVQEECY 130
          :||: | :|| |::|| |::||:||||| ||| ||||:|||||
Db      71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECY 130

Qy      131 KLVNC SIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD SLMEKIGPNM 190
          :|::| :|: |||| |::| | | ||:: |::|| |::||: :| |: :|::|
Db      131 RLDICGVARSNPEAIGEVVQVPAHFNPYRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

Qy      191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLRLNLRGEEDSPSHI 239
          :||:| | | : : | | | : :|| : |::
Db      191 ETLFQLLQNKHCPQGSNQGPNAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241

```

RESULT 13

US-10-116-051-10

; Sequence 10, Application US/10116051

```
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10
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```
Query Match          52.1%; Score 660.5; DB 13; Length 204;
Best Local Similarity 60.8%; Pred. No. 7.1e-59;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
```

```
Qy      11 LVISASATHEAEQNDSVSPRKS RVAAQNSAEVVRCLNSALQVGC GAFACLENSTCDTDGM 70
      ||:  :|| : :  :: |||::| : :  ::| |||| || |||| |||||
Db      12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy      71 YDICKSFLYSAAKFDTQ GKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECY 130
      :|||: | :|| | :||| | ||||: ||||| ||| | ||||: |||||
Db      71 HDICQLFFHTAATFNTQ GKTFVKESLR CIANGVTSKV FQTIRRCGVFQRMISEVQEECY 130

Qy      131 KLNVC SIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDTVSTIRD SLMEKIGPNM 190
      :|::| :|: | |||| | |||: | || | |||: |::|| | ||: ||: :| | : :||:|
Db      131 RLDICGVARSNPEAIGEVVQVPAHF PNRYYSTLLQSL LACDEETVAVVRAGLVARLGPD 190

Qy      191 ASLFHILQTDHCAQ 204
      :|| :|| || |
Db      191 ETLFQLLQNKHCPQ 204
```

RESULT 14

US-09-361-736-9

```
; Sequence 9, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
```

```

; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-9

```

```

Query Match          49.5%; Score 628; DB 9; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

```

```

Qy      28 SPRKSRVAAQNSAEVVRCLNSALQVGCFAFACLENSTCDTDGMYDICKSFLYSAKFDTQ 87
      ||| :| :| : :| |||| ||||| |||||:||||:||||:|:|:|: |||||
Db      1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAKFDTQ 60

Qy      88 GKAFVKESLKCANGVTSTKVFLAIRRCSTFORMIAEVQEECYSKLNVCSIAKRNPEAITE 147
      || |||||:||||| ||||:|:|:|:|||||:|:|:|: ||||| |
Db      61 GKTFFVKESLKCANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy      148 VVQLPNHFSNRYYNRLVRSLLCEDTDTVSTIRDSLMEKIGPNMASLFHIL 197
      | |:| | |||:|:| || |||| :| |: :| | | :|
Db      121 VAQVPSQFPNRYYSTLLQSLLTCEDETVQVRAGLVSRLEPEMGVLFQLL 170

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RESULT 15

US-10-418-226-9

```

; Sequence 9, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736

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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9
```

```
Query Match          49.5%; Score 628; DB 14; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;
```

```
Qy      28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
      ||| :| :| : :| |||| ||||| |||||:||||:||||:|:|:|: |||||
Db      1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy      88 GKAFVKESLKCIANGVT SKVFLAIRRCSTFORMIAEVQEECYSKLNVCSI AKRNPEAITE 147
      || ||||| |||||:||||| |||||:|:|:|: ||||| |||||:|:|:|: |||||
Db      61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy      148 VVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRDSLMEKIGPNMASLFHIL 197
      | |:|: | ||||: |:||| ||||| :| |: :| | | | :|
Db      121 VAQVPSQFPNRYYSTLLQSLLTCEDETV EQVRAGLVSRLEPEMGVLFQLL 170
```

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Job time : 153 secs
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